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UNDER 37 CFR 1.8(a)

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9 JUNE 2004
HUESCHEN AND SAGE

Dated: 9 JUNE 2004

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Applicant : Burkhard SCHULZ
Serial No. : 09/914,220
Filed : January 31, 2002
Title : DNA SEQUENCE OF A PROTEIN THAT IS SIMILAR TO FKBP.
Art Unit : 1638
Examiner : Stuart F. BAUM, Esq.

Honorable Commissioner of Patents and Trademarks
Alexandria, VA 22313

RESPONSE AND ELECTION UNDER 37 CFR § 1.142

Sir:

Responsive to the Office Action, a Restriction Requirement, dated March 11, 2004, as to which the period for response has been extended by two (2) months by payment of the appropriate fee, the Applicants rebut the Office assertion that the claims lack a single inventive concept. The Office basis for at least a portion of the Restriction Requirement is the disclosure of Xu, et al., which the Office contends teach a nucleic acid sequence from *Vicia faba* which comprises a fragment of the instant SEQ ID No. 1. The Applicants submit that Xu, et al. disclose an amino acid sequence of an FKBP-12 protein, a protein which is distinct from the protein encoded by the instant claimed nucleic acid sequences. To substantiate this

understanding, the Applicants point out that the amino acid sequence of the FKBP-12 protein of *Vicia faba* is compared to orthologues from multiple species in Figure 1. of Xu, et al., including *Arabidopsis thaliana*, the species from which the instant FKBP-like protein was identified. The FKBP-12 protein from *Arabidopsis thaliana* is demonstrated to have 81% identity to the FKBP-12 protein from *Vicia faba*, which is described to be typical of most well-conserved proteins in higher plants (see Results section). The Applicants presently submit a pairwise sequence alignment of the FKBP-12 amino acid sequence disclosed in Xu, et al. (query sequence) and the instant amino acid sequence of SEQ ID No. 3, both from *Arabidopsis thaliana*. These non-analogous proteins exhibit 33% identity at the amino acid level and do not possess a common fragment, as indicated by the Office. Thus, from the teaching of Xu, et al. one skilled in the art would conclude that these proteins are distinct. Therefore, the Office basis for concluding that Restriction Groups I-IV do not possess a common special technical feature is not made out in the evidence of record and, consequently, the Restriction Requirement in view of Xu, et al. is unfounded.

The Applicants submit that the single inventive concept of the instant invention is in the novel protein described in SEQ ID No. 3, which is encoded by the claimed nucleic acid sequence in SEQ ID NOs. 1 and 2. Further, the subject matter of claims in Restriction Groups III and IV is drawn to species homologues of the claimed protein which demonstrate significant homology to the subject matter of Group II. Claims in Restriction Groups VI and VII are drawn to specific uses of the claimed nucleic acid sequence. Thus, the subject matter of each restriction group is connected by this common special technical feature, namely, the nucleotides for generating a novel protein, that protein, and the use of nucleotides encoding that protein. Consequently, reconsideration of the Restriction requirement is respectfully requested.

In the event the above arguments are not found persuasive, the Applicants elect, with traverse, to prosecute Claim(s) 14-15, 17-20 and 23-26, directed to Group II of the Restriction Requirement. The elected claims are drawn to the nucleic acid sequence of SEQ ID No: 2, vectors, methods for producing transgenic plants, transgenic plants and seeds. In addition, the Applicants elect to prosecute, in combination with the invention of Group II, Method Claim 21 of Restriction group VI, involving the use of the elected nucleic acid sequence.

The Office may withdraw the non-elected subject matter without prejudice to their rejoinder during later examination and/or prosecution in a divisional application.

The Applicants respectfully submit that by merely withdrawing the non-elected subject matter pending notification of allowable subject matter, the Applicants distinctly and affirmatively identify subject matter which they assert, upon examination will be found a part of the claimed invention. The Applicants reassert their right to rejoin non-elected claims upon the identification of allowable subject matter.

* * * * *

Accordingly, entry of the present Election into the record of this application, and swift and favorable consideration of the instant application is respectfully solicited.

Respectfully submitted,

THE FIRM OF HUESCHEN AND SAGE

By: 
G. PATRICK SAGE

Dated: June 9, 2004
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Enclosure: Certified Check, in the amount of \$420.00 (four hundred twenty dollars) for two (2) month extension, BLASTp program pairwise alignment, one (1) page and Postal Card Receipt.

THE COMMISSIONER IS HEREBY AUTHORIZED TO CHARGE ANY FURTHER OR ADDITIONAL FEES WHICH MAY BE REQUIRED (DUE TO OMISSION, DEFICIENCY, OR OTHERWISE), OR TO CREDIT ANY OVERPAYMENT, TO DEPOSIT ACCOUNT NO. 08,3220.

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

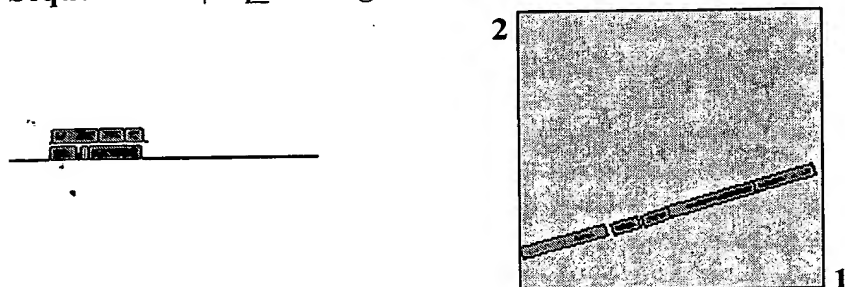
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

Sequence 1 lcl|seq_1 Length 112 (1 .. 112)

Sequence 2 lcl|seq_2 Length 365 (1 .. 365)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 47.8 bits (112), Expect = 6e-05
Identities = 36/109 (33%), Positives = 54/109 (49%), Gaps = 5/109 (4%)

Query: 3 VEKQVIRPGNGPKPAPGQTVTVHCIGFGKDGDL SQKFWSTKDEGQKPF SFQIGK-GAVIK 61
V KQ+I+ G+G KP+ T +H + K+ KF T E Q+P +GK +
Sbjct: 51 VSKQIIKEGHGSKPSKYSTCFLHYRAWTKNS--QHKFEDTWHE-QQPIELVLGKEKKELA 107

Query: 62 GWDFGVIGMQIGEVARIRCSSDYAYG-AGGFPAWGIQPN SVIDFEIEVI 109
G GV M+ GE A + + AY G F + P + + +E+EVI
Sbjct: 108 GLAIGVASMKSGERALVHVGWELAYGKEGNFSFPNVPPMADLLYEVEVI 156

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda K H
0.319 0.142 0.451

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 339
Number of Sequences: 0
Number of extensions: 38
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 0